

Sequence Comparison C

RESULT 1

JN0621

G protein-coupled receptor type B - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000

C;Accession: JN0621

R;Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.

Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A;Title: Identification of novel members of G-protein coupled receptor superfamily expressed in bovine taste tissue.

A;Reference number: JN0621; MUID:93326166

A;Accession: JN0621

A;Molecule type: mRNA

A;Residues: 1-350 <MAT>

A;Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711

A;Experimental source: tongue taste papillae

C;Comment: This protein is involved in modulating taste sensitivity or regeneration of taste cells.

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

F;42-66/Domain: transmembrane #status predicted <TM1>

F;80-99/Domain: transmembrane #status predicted <TM2>

F;114-135/Domain: transmembrane #status predicted <TM3>

F;154-175/Domain: transmembrane #status predicted <TM4>

F;200-222/Domain: transmembrane #status predicted <TM5>

F;242-265/Domain: transmembrane #status predicted <TM6>

F;284-306/Domain: transmembrane #status predicted <TM7>

F;6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.1%; Score 1620; DB 2; Length 350;

Best Local Similarity 86.0%; Pred. No. 1.1e-131;

Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

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Qy      1 MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
          |||:| ||||| ||||| |||:|||||:|||||:|:||||| || || |:|||||
Db      1 MAVEQNQSTDYYYEENEMNDTHDYSQYEVICIKKEVRKFAKVFLPAFFTIAFIIGLAGNS 60

Qy     61 MVVAIYAYYKKQRTKTDVYIILNLAVADLLLLFTLPFWAVNAVHGWLKGIMCKITSALYT 120
          ||||| |||||:||||| ||||| ||||| ||||| ||||| |||||:|||||
Db     61 TVVAIYAYYKKRRTKTDVYIILNLAVADLFLFTLPFWAVNAVHGWLKGIMCKVTSALYT 120

Qy    121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFYTVND 180
          :||||| ||||| ||| ||| ||||| |||||:|||||:||||| ||||| |||||
Db    121 VNFVSGMQFLACISTDRYWAVTKAPSQSGVGKPCWVICFCVWVAAILLSIPQLVFYTVNH 180

Qy    181 NARCIPIFPYRLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
          |||:|||| :||||| |||:|||||:||||| ||||| |||||:||||| |||||
Db    181 KARCVPFPYHLGTSMKASIQILEICIGFIIPFLIMAVCYFITAKTLIKMPNIKKSQPLK 240

Qy    241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSLNLP 300
          || ||||| ||||| |||||:||||| ||||| ||||| |||||:||||| |||||
Db    241 VLFTVVIVFIVTQLPYNIVKFCQAIDIIYSLITDCDMSKRMDVAIQITESIALFHSLNLP 300

Qy    301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPDSEGPTEPTSTFSI 350
          :||||| |||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 VLYVFMGTSFKNYIMKVAKKYGSWRRQRQNVEEIPFESEDATEPTSTFSI 350

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